

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2003, 23:44:32 ; Search time 1168.39 Seconds
(without alignments)
471.288 Million cell updates/sec

Title: US-09-913-524-33

Perfect score: 34

Sequence: 1 aggcctcggaggaaacnctgccaatgccaact 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```
EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hic: *
9: gb_estl: *
10: gb_est2: *
11: gb_hic: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inw: *
20: em_gss_pln: *
21: em_gss_vit: *
22: em_gss_fun: *
23: em_gss_man: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rtd: *
```

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	97.1	251	14	T29423 EST79588 Hu
2	33	97.1	364	10	AW951334 EST363404
C 3	33	97.1	501	9	AI128256 qc33h05.x
C 4	33	97.1	884	13	BI520936
C 5	33	97.1	899	9	AL568487
6	33	97.1	924	9	AL540575

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

C 7	31.4	92.4	599	9	AI220927
C 8	29	85.3	548	14	BQ013783
C 9	26.6	78.2	510	9	AI885743
10	25	73.5	399	12	BE758121
11	25	73.5	464	13	BI849730
12	25	73.5	466	9	AA234854
13	25	73.5	561	12	BE721322
14	25	73.5	1074	13	BM460913
15	25	73.5	1118	13	BM461343
C 16	24	70.6	613	10	AW55078
C 17	24	70.6	641	13	BI186150
C 18	23.4	68.8	640	12	BG872889
C 19	23.4	68.8	659	13	BI183158
C 20	23.4	68.8	705	13	BI182159
21	23.4	68.8	1172	13	BM461317
C 22	22.6	66.5	582	14	C87829
C 23	22.4	65.9	649	13	BI181741
24	22.4	65.9	978	14	BM804780
C 25	22	64.7	629	13	BM665951
C 26	22	64.7	1521	13	BM563318
27	21.8	64.1	1129	13	BM461356
28	21.2	62.4	845	13	BI857862
C 29	21	61.8	446	9	AA613867
30	20.8	61.2	343	17	B81629
31	20.8	61.2	485	14	BM838500
32	20.8	61.2	539	13	BM127079
33	20.8	61.2	575	17	AZ812884
34	20.8	61.2	800	13	BI087023
35	20.8	61.2	927	9	AL532730
36	20.6	60.6	425	14	N41644
C 37	20.6	60.6	716	17	AZ624232
38	20.6	60.6	775	14	BQ571532
C 39	20.4	60.0	503	12	BG625183
C 40	20.4	60.0	669	17	AG148285
41	20.4	60.0	914	14	BQ433546
42	20.4	60.0	976	13	BI770561
C 43	20.4	60.0	1149	14	BM806299
44	20.2	59.4	392	13	BM041782
C 45	20.2	59.4	466	10	AW475765

ALIGNMENTS

RESULT 1	T29423	EST79588	Human Placenta	451 bp	mRNA	linear	EST 06-SEP-1995
LOCUS	T29423	EST79588	Human Placenta	451 bp	mRNA	linear	EST 06-SEP-1995
DEFINITION	T29423	EST79588	Human Placenta	451 bp	mRNA	linear	EST 06-SEP-1995
ACCESSION	T29423	EST79588	Human Placenta	451 bp	mRNA	linear	EST 06-SEP-1995
VERSION	T29423	EST79588	Human Placenta	451 bp	mRNA	linear	EST 06-SEP-1995
KEYWORDS	T29423	EST79588	Human Placenta	451 bp	mRNA	linear	EST 06-SEP-1995
SOURCE	T29423	EST79588	Human Placenta	451 bp	mRNA	linear	EST 06-SEP-1995
ORGANISM	T29423	EST79588	Human Placenta	451 bp	mRNA	linear	EST 06-SEP-1995
REFERENCE	T29423	EST79588	Human Placenta	451 bp	mRNA	linear	EST 06-SEP-1995

AUTHORS TITLE JOURNAL COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L14M1405 row: f column: 10
High quality sequence start: 2
High quality sequence stop: 726.
High quality sequence stop: 726.

FEATURES source

1. .884
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5163273"
/clone_lib="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

BASE COUNT 175 a 231 c 327 g 151 t
ORIGIN

Query Match 97.1%; Score 33; DB 13; Length 884;
Best Local Similarity 97.1%; Pred. No. 0.1;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGCTCCGGAGGAACGCTGCCATGCCAACT 34
|||||
Db 458 AGGCTCCGGAGGAACGCTGCCATGCCAACT 425

RESULT 5 AL568487/c LOCUS

DEFINITION AL568487 LTI_FL002_P11 Homo sapiens cDNA clone CS0DE002YE07 3 prime
; mRNA sequence.

ACCESSION AL568487
VERSION AL568487.1 GI:12922875
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 899)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL

COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
Location/Qualifiers

1. .899
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DE002YE07"
/clone_lib="LTI_FL002_P11"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
; Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
<http://fulllength.invitrogen.com>"

BASE COUNT 184 a 229 c 318 g 159 t 9 others
ORIGIN

Query Match 97.1%; Score 33; DB 9; Length 899;
Best Local Similarity 97.1%; Pred. No. 0.1;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGCTCCGGAGGAACGCTGCCATGCCAACT 34
|||||
Db 458 AGGCTCCGGAGGAACGCTGCCATGCCAACT 425

RESULT 6 AL540575 LOCUS

DEFINITION AL540575 LTI_FL002_P11 Homo sapiens cDNA clone CS0DE002YE07 5 prime
; mRNA sequence.

ACCESSION AL540575
VERSION AL540575.1 GI:12870853
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 924)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL

COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
Location/Qualifiers

1. .924
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DE002YE07"
/clone_lib="LTI_FL002_P11"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
; Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
<http://fulllength.invitrogen.com>"

BASE COUNT 153 a 307 c 299 g 165 t
ORIGIN

Query Match 97.1%; Score 33; DB 9; Length 924;
Best Local Similarity 97.1%; Pred. No. 0.1;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGCTCCGGAGGAACGCTGCCATGCCAACT 34
|||||
Db 838 AGGCTCCGGAGGAACGCTGCCATGCCAACT 871

RESULT 7 AI220927/c LOCUS

DEFINITION AI220927 Soares_placenta_8to9weeks_2Nduh18to9W Homo sapiens cDNA
9908a11.x1

clone IMAGE:1758908 3' similar to gb:M13981 INH1BIN ALPHA CHAIN
 PRECURSOR (HUMAN);, mRNA sequence.
 A1220927 A1220927.1 GI:3803130
 EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 599)
 NC1-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LLNL: contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 761 Std Error: 0.00
 Seq primer: 40UP from Gibco
 High quality sequence stop: 379.
 Location/Qualifiers
 1..599
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1758908"
 /dev_stage="Two placenta: one from 8 weeks and another
 from 9 weeks post conception"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: placenta; Vector: pT73D (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTTACCAATCTGAAGTGGAGCGCGCGATTCTTTTCTTTTCTTTT 3']
 double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library constructed by Bento Soares and
 M.Fatima Bonaldo."

FEATURES

source

BASE COUNT 135 a 142 c 203 g 115 t 4 others
 ORIGIN
 Query Match 92.4%; Score 31.4; DB 9; Length 599;
 Best Local Similarity 94.1%; Pred. No. 0.34;
 Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 AGGCCTCCGAGAACCGCTGCCATGCCAACT 34
 |||||
 Db 540 AGGCCTCCGAGAACCGCTGCCATGCCAACT 507
 |||||

RESULT 8
 B0013783/C
 LOCUS B0013783 548 bp mRNA linear EST 26-MAR-2002
 DEFINITION UI-1-BCL1p-alb-q-08-0-UI.s1 NC1-CGAP_P13 Homo sapiens cDNA clone
 UI-1-BCL1p-alb-q-08-0-UI 3', mRNA sequence.
 B0013783
 ACCESSION B0013783
 VERSION B0013783.1 GI:19738684
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 548)
 NC1-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Steven Brown
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source

1..548
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UI-1-BCL1p-alb-q-08-0-UI"
 /clone_lib="NC1-CGAP_P13"
 /tissue_type="placenta"
 /dev_stage="8-9 weeks"
 /lab_host="DH10B (L.C. Technologies)"
 /note="Organ: Placenta; Vector: pT73-Pac (Pharmacia) with
 a modified polylinker; Site_1: EcoR I; Site_2: Not I;
 NC1-CGAP_P13 is a subcloned cDNA library constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pT73-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tags for this library are GA, AGGA. For
 additional information, contact: Bento Soares,
bento-soares@uiowa.edu
 TAG_LifB-UI-1-BCL1p
 TAG_TISSUE=placenta human 8 week
 TAG_SEQ=GA"

BASE COUNT 122 a 123 c 185 g 118 t
 ORIGIN

Query Match 85.3%; Score 29; DB 14; Length 548;
 Best Local Similarity 96.7%; Pred. No. 2.3;
 Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 CTCGGAGGAAACCGCTGCCATGCCAACT 34
 |||||
 Db 548 CTCGGAGGAAACCGCTGCCATGCCAACT 519
 |||||

RESULT 9
 A1885743/C
 LOCUS A1885743 510 bp mRNA linear EST 07-MAR-2000
 DEFINITION w161a07.x1 NC1-CGAP_P1025 Homo sapiens cDNA clone IMAGE:2429364 3',
 similar to gb:M13981 INH1BIN ALPHA CHAIN PRECURSOR (HUMAN);, mRNA
 sequence.
 A1885743
 ACCESSION A1885743
 VERSION A1885743.1 GI:55909407
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 510)
 NC1/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute / National Institute of Neurological
 Disorders and Stroke, Brain Tumor Genome Anatomy Project
 (CGAP/BTGP), Tumor Gene Index
 JOURNAL Unpublished (1998)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
 Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NC1-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 1166 \$id Error: 0.00
 Seq primer: -400p from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

1..510
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="2429364"
 /clone_lib="NCI_CCAP_Brn25"
 /tissue_type="anaplastic oligodendroglioma"
 /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA was primed with a Not 1 - oligo(dT) primer [5' TGTTACCAATCGAAGTGGAGCGCGCATAGGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not 1 and cloned into the Not 1 and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Horaldo."

BASE COUNT 126 a 144 c 141 g 95 t 4 others
 ORIGIN

Query Match 78.2%; Score 26.6; DB 9; Length 510;
 Best Local Similarity 85.3%; Pred. No. 16;
 Matches 29; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGGCTCGGAGAACCGNTGCCATGCCAACT 34
 ||||| || ||||| ||||| ||||| |||||
 Db 441 AGGCTCGGAGAACCGNTGCCATGCCAACT 408

RESULT 10

BE758121

LOCUS BE758121 399 bp mRNA linear EST 25-APR-2001
 DEFINITION 212839 MARC 2B0V Bos taurus cDNA 5', mRNA sequence.

ACCESSION BE758121

VERSION BE758121.1 GI:10172185

KEYWORDS EST.

SOURCE cow.

ORGANISM

Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.

REFERENCE

AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Perlea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

TITLE

JOURNAL 21180013
 MEDLINE 21180013
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCTCAGTCAGCAGC
 Plate: 56 row: I column: 16
 Seq primer: ATTTAGGTGACACTATAG.

Location/Qualifiers

1..399

/organism="Bos taurus"

FEATURES

source

/db_xref="taxon:9913"
 /clone_lib="MARC 2B0V"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: SalI;
 Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
 BASE COUNT 46 a 167 c 108 g 78 t
 ORIGIN

Query Match 73.5%; Score 25; DB 12; Length 399;
 Best Local Similarity 82.4%; Pred. No. 55;
 Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AGGCTCGGAGAACCGNTGCCATGCCAACT 34
 ||||| || ||||| || ||||| ||||| |||||
 Db 278 AGGCTCGGAGAACCGNTGCCATGCCAACT 311

RESULT 11

BI849730

LOCUS BI849730 464 bp mRNA linear EST 04-OCT-2001
 DEFINITION 477654 MARC 2B0V Bos taurus cDNA 5', mRNA sequence.

ACCESSION BI849730

VERSION BI849730.1 GI:15962249

KEYWORDS EST.

SOURCE cow.

ORGANISM

Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.

REFERENCE

AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Perlea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.

1 (bases 1 to 464)

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGTCAGCAGC

Plate: 102 row: L column: 5

Seq primer: ATTTAGGTGACACTATAG.

Location/Qualifiers

1..464

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 2B0V"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: SalI;
 Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

BASE COUNT 73 a 172 c 126 g 93 t

ORIGIN

Query Match 73.5%; Score 25; DB 13; Length 464;

Best Local Similarity 82.4%; Pred. No. 58;

Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgaaps-r@mail.nih.gov
 Tissue Procurement: Aaron Hsueh
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1AM12145 row: f column: 03
 High quality sequence start: 16
 High quality sequence stop: 739.

FEATURES

source

1. .1074
 Location/Qualifiers
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:5504258"
 /clone_lib="NCL_CGAP_Ov44"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: ovary, PMSG-treated; Vector:
 PCMV-SPORT6.ccdB; Site_1: EcoRV; Site_2: NotI; Cloned
 unidirectionally. Primer: Oligo dT. Average insert size
 2.2 kb. Library constructed by Life Technologies. Note:
 this is a NCL_CGAP Library."
 176 a 343 c 319 g 232 t 4 others

BASE COUNT
 ORIGIN

Query Match 73.5%; Score 25; DB 13; Length 1074;

Best Local Similarity 82.4%; Pred. No. 71;
 Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AGCCCTCCGAGGAGAACCGTGGCCATGCCCAACT 34
 ||||| ||||| ||||| ||||| ||||| ||
 Db 815 AGCCCTCCGAGGAGAACCGTGGCCATGCCCTTCT 848

RESULT 15

BX461343

LOCUS

DEFINITION HM461343 1118 bp mRNA linear EST 05-FEB-2002
 AGENCOURT_6419744 NCL_CGAP_Ov44 Mus musculus cDNA clone
 IMAGE:5504094 5', mRNA sequence.

ACCESSION

BX461343

VERSION

EST.

KEYWORDS

house mouse.

SOURCE

Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC <http://mqc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaaps-r@mail.nih.gov
 Tissue Procurement: Aaron Hsueh
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1AM12144 row: o column: 07
 High quality sequence stop: 672.

FEATURES

source

1. .1118
 Location/Qualifiers
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:5504094"
 /clone_lib="NCL_CGAP_Ov44"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: ovary, PMSG-treated; Vector:
 PCMV-SPORT6.ccdB; Site_1: EcoRV; Site_2: NotI; Cloned
 unidirectionally. Primer: Oligo dT. Average insert size

2.2 kb. Library constructed by Life Technologies. Note:
 this is a NCL_CGAP Library."
 BASE COUNT 179 a 372 c 323 g 244 t

ORIGIN

Query Match 73.5%; Score 25; DB 13; Length 1118;
 Best Local Similarity 82.4%; Pred. No. 72;
 Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AGCCCTCCGAGGAGAACCGTGGCCATGCCCAACT 34
 ||||| ||||| ||||| ||||| ||||| ||
 Db 793 AGCCCTCCGAGGAGAACCGTGGCCATGCCCTTCT 826

Search completed: March 11, 2003, 10:26:00
 Job time : 1171.39 secs